

<!--StartFragment-->RESULT 1

HNL_MANES

ID HNL_MANES Reviewed; 258 AA.
 AC P52705;
 DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
 DT 23-JAN-2007, sequence version 3.
 DT 24-JUL-2007, entry version 45.
 DE (S)-acetone-cyanohydrin lyase (EC 4.1.2.39) ((S)-hydroxynitrile lyase)
 DE ((S)-hydroxynitrilase) (Oxynitrilase).
 GN Name=HNL;
 OS Manihot esculenta (Cassava) (Manioc).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
 OC Manihoteae; Manihot.
 OX NCBI_TaxID=3983;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND PROTEIN SEQUENCE OF 2-37 AND 169-192.
 RC TISSUE=Cotyledon;
 RX MEDLINE=94263231; PubMed=8203915; DOI=10.1006/abbi.1994.1267;
 RA Hughes J., Carvalho F.J.P.D.C., Hughes M.A.;
 RT "Purification, characterization, and cloning of alpha-hydroxynitrile
 RT lyase from cassava (Manihot esculenta Crantz).";
 RL Arch. Biochem. Biophys. 311:496-502(1994).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX PubMed=11173464; DOI=10.1107/S0907444900015766;
 RA Lauble H., Foerster S., Miehllich B., Wajant H., Effenberger F.;
 RT "Structure of hydroxynitrile lyase from Manihot esculenta in complex
 RT with substrates acetone and chloroacetone: implications for the
 RT mechanism of cyanogenesis.";
 RL Acta Crystallogr. D 57:194-200(2001).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS), AND MUTAGENESIS OF SER-80.
 RX PubMed=11316882; DOI=10.1110/ps.01301;
 RA Lauble H., Miehllich B., Foerster S., Wajant H., Effenberger F.;
 RT "Mechanistic aspects of cyanogenesis from active-site mutant Ser80Ala
 RT of hydroxynitrile lyase from Manihot esculenta in complex with acetone
 RT cyanohydrin.";
 RL Protein Sci. 10:1015-1022(2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX PubMed=11742123; DOI=10.1110/ps.ps.33702;
 RA Lauble H., Miehllich B., Foerster S., Kobler C., Wajant H.,
 RA Effenberger F.;
 RT "Structure determinants of substrate specificity of hydroxynitrile
 RT lyase from Manihot esculenta.";
 RL Protein Sci. 11:65-71(2002).
 CC -!- FUNCTION: Involved in cyanogenesis, the release of HCN from

CC injured tissues. Decomposes a varieties of (R) or (S) cyanohydrins
 CC into HCN and the corresponding aldehydes and ketones. The natural
 CC substrate of this enzyme is (S)-acetone cyanohydrin.
 CC -!- CATALYTIC ACTIVITY: 2-hydroxyisobutyronitrile = cyanide + acetone.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily.
 CC Hydroxynitrile lyase family.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; Z29091; CAA82334.1; -; mRNA.
 DR PDB; 1DWO; X-ray; A/B=1-258.
 DR PDB; 1DWP; X-ray; A/B=1-258.
 DR PDB; 1DWQ; X-ray; A/B=1-258.
 DR PDB; 1E89; X-ray; A/B=1-258.
 DR PDB; 1E8D; X-ray; A/B=1-258.
 DR PDB; 1EB8; X-ray; A/B=1-258.
 DR PDB; 1EB9; X-ray; A/B=1-258.
 DR BioCyc; MetaCyc:MONOMER-6902; -.
 DR GO; GO:0046991; F:hydroxynitrilase activity; IEA:EC.
 DR InterPro; IPR000073; AB_hydrolase_1.
 DR Pfam; PF00561; Abhydrolase_1; 1.
 PE 1: Evidence at protein level;
 KW 3D-structure; Direct protein sequencing; Lyase.
 FT INIT_MET 1 1 Removed.
 FT CHAIN 2 258 (S)-acetone-cyanohydrin lyase.
 FT /FTId=PRO_0000084018.
 FT ACT_SITE 80 80 By similarity.
 FT ACT_SITE 208 208 By similarity.
 FT ACT_SITE 236 236 By similarity.
 FT MUTAGEN 80 80 S->A: Loss of activity.
 FT STRAND 4 8
 FT HELIX 15 18
 FT HELIX 21 27
 FT STRAND 31 35
 FT HELIX 47 49
 FT HELIX 53 56
 FT HELIX 58 66
 FT STRAND 73 79
 FT HELIX 82 92
 FT HELIX 93 95
 FT STRAND 96 104
 FT STRAND 109 111
 FT HELIX 115 123
 FT STRAND 131 136
 FT STRAND 142 147
 FT HELIX 150 156
 FT HELIX 163 172

FT	HELIX	180	184
FT	TURN	191	193
FT	HELIX	194	196
FT	STRAND	197	203
FT	STRAND	208	210
FT	HELIX	212	221
FT	STRAND	225	229
FT	HELIX	237	240
FT	HELIX	242	256
SQ	SEQUENCE	258 AA;	29372 MW; 98ABA050AC8AF1C5 CRC64;

Query Match 100.0%; Score 1360; DB 1; Length 258;
 Best Local Similarity 100.0%; Pred. No. 9.1e-102;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVTAHFVLIHTICHGAWIWHKLKPALERAGHKVTALDMAASGIDPRQIEQINSFDEYSEP	60
Db	1	MVTAHFVLIHTICHGAWIWHKLKPALERAGHKVTALDMAASGIDPRQIEQINSFDEYSEP	60
Qy	61	LLTFLEKLPQGEKVIIVGESACAGLNIAAADRYVDKIAAGVFHNSLLPDTVHSPSYTVEK	120
Db	61	LLTFLEKLPQGEKVIIVGESACAGLNIAAADRYVDKIAAGVFHNSLLPDTVHSPSYTVEK	120
Qy	121	LLESFPDWRDTEYFTFTNITGETITTMKLGFLVLLRENLF TKCTDGEYELAKMVMRKGS LF	180
Db	121	LLESFPDWRDTEYFTFTNITGETITTMKLGFLVLLRENLF TKCTDGEYELAKMVMRKGS LF	180
Qy	181	QNVLAQRPKFTEKGYGSIKKVYIWDQDKIFLPDFQRWQIANYPDKVYQVQGGDHKLQL	240
Db	181	QNVLAQRPKFTEKGYGSIKKVYIWDQDKIFLPDFQRWQIANYPDKVYQVQGGDHKLQL	240
Qy	241	TKTEEVAHILQEVADAYA	258
Db	241	TKTEEVAHILQEVADAYA	258

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